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Genetic signature of a recent southern range shift in *Glossina tachinoides* in East Burkina Faso

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ABSTRACT

In the eastern part of Burkina-Faso, the riverine tsetse fly, *Glossina tachinoides* Westwood, transmits African animal trypanosomosis that constitute a major constraint to sub-Saharan agriculture. To organize an efficient vector control campaign against this vector, it is crucial to identify and target isolated populations in order to prevent any risk of reinvasion. Previous entomological data using traps in this part of the country have suggested that *G. tachinoides* has now become discontinuously distributed with a western and an eastern tsetse belt. In this paper, we studied population genetics on *G. tachinoides* trapped in two sites, separated by 150 kms, on the western and eastern sides of this "gap". We found that a significant differentiation does exist between the two sites and that it is fairly above than what was expected given the geographic distance. A comparison between observed and expected differentiation allowed estimating that the total separation between these two sites could have occurred around 10 years ago (i.e. between 1 and 21 years), which is in line with the dates of environmental changes that occurred in this area. This result will help the national PATTEC project to organize the tsetse eradication in this area.

1. Introduction

Tsetse flies (Diptera: Glossinidae) are the cyclical vectors of African human (HAT) and animal (AAT) trypanosomoses in subsaharan Africa. AAT is a major obstacle to the development of more efficient and sustainable livestock production systems in West Africa, and vector control remains widely used to lower this constraint. For HAT, vector control is an important complement to case detection and treatment, because reducing host/vector contact can rapidly halt human trypanosomiasis transmission (Rogers, 1979; Laveissière and Penchenier, 2005). Also, in the absence of any chemoprophylaxis available, vector control also remains the only available strategy capable of protecting human individuals from acquiring infection (Solano et al., 2010). Tsetse populations may be reduced using a variety of techniques, including insecticide impregnated traps and targets, live-baits, sequential aerial spraying, and sterile male releases (Challier et al., 1977; Cuisance et al., 1984; Vreysen et al., 2000; Kgori et al., 2006; Bouyer et al., 2010; Torr and Solano, 2010). A prerequisite to any vector control campaign aiming at eradication is to identify and target isolated populations because then, control measures can be implemented without risk of reinvasion. If not isolated, populations can be isolable by applying barriers, for instance barriers of insecticide impregnated traps and targets (Politzar and Cuisance, 1983). Application of population genetic techniques can help understanding and quantifying gene flows between subpopulations as an indirect measure of dispersal (Gooding and Krafsur, 2005), and can be used as a tool in decision making for control strategies (Solano et al., 2010; Kaba et al., 2012).

In Burkina-Faso, two riverine tsetse flies, *Glossina palpalis gambiensis* (*G. p. g*) Vanderplank and *Glossina tachinoides* (*G. t*) Westwood, occur in the southern half of the country, where they transmit AAT (Bouyer et al., 2009). In the western part of the country, *G. p. gambiensis* occurs as well as *G. tachinoides*. In the eastern part of the country only *G. tachinoides* has been caught (Courtin et al., 2010). During the update of the northern distribution limit of tsetse flies in Burkina Faso, entomological data using traps have suggested that *G. tachinoides* has now become discontinuously distributed with a western and an eastern tsetse belt, between which no fly could be caught anymore (Courtin et al., 2010).

However, it is well known that an absence of tsetse in traps does not demonstrate an absence of tsetse, since a significant part of tsetse attracted to traps may not enter it, especially when they occur at low densities (Rayaisse et al., 2010, 2012). In the present study, we therefore used population genetics on *G. tachinoides* captured on the western and eastern sides of this "gap", to check if ge-

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netic differentiation increased in a magnitude compatible with a progressive disappearance of gene flow between these two populations as a consequence of the droughts of 1970s and the population growth increase in the area (Laveissere, 1976; Courtin et al., 2010). This gap constitutes critical information for the organization of the tsetse eradication campaign that is planned by the Pan African Tsetse and Trypanosomosis Eradication Campain (PATTEC) project of Burkina Faso.

2. Material and methods

2.1. Study area

The study area is located in the Center-East of Burkina Faso. In Bitou, on the eastern side, landscape is constituted by savannahs degraded by farming and human settlements. In Pama, on the western side, the vegetation is more conserved and denser, due to the fact that the main part of the area is protected and classified as a national park. Bitou and Pama are 150 km away (Fig. 1). Between these two sites, only in rare places tsetse may still occur, along the Nouhao and the Kompienga rivers. However, all this area is totally occupied by man for farming, with riverine vegetation no longer present, hence a poor probability for tsetse presence in the area located between Bitou and Pama.

2.2. Sampling and genotyping

Tsetse flies were sampled using respectively five and nine biconical traps in May 2012 in the two sites, Bitou (91 flies, 52 females and 39 males) and Pama (264 flies, 132 females and 132 males). Distance between traps varies between 320 m and 1.94 kms in Bitou and between 60 m and 1.96 kms in Pama. *G. tachinoides* were collected from the traps, counted and separated by sex. Three legs were removed from each fly and put in individual labeled dry microtubes.

Selection of flies to be genotyped followed the following steps. All cages (of a trap) containing a fly was selected. Within the cage, the quality of the fly was taken into account and only intact, not dry flies with six legs and both wings present were selected for genotyping.

A mean of 14 flies per trap (ranging from 5 to 25) in Bitou and 6.2 (ranging from 1 to 21) in Pama were genotyped, giving a total of 60 (Bitou site, 66% of collected flies, 23 males and 37 females) and 60 (Pama site, 23% of collected flies, 22 males and 38 females). *G. tachinoides* were genotyped at six polymorphic microsatellite loci: XpGp13, pGp24, pGp28, XB104, C102 and GPCAG with X signifying that the locus is heterosomal and thus haploid in males. Detailed procedures of genotyping have been described elsewhere (Solano et al., 2009).

Prior to genotyping, a simple diagnostic PCR based on ITS 1 DNA (Dyer et al., 2008), that allows distinguishing between *G. p. gambiensis* and *G. tachinoides* was realised on all the samples.

2.3. Data analyses

In order to determine the smallest relevant population units we undertook a hierarchical analysis with HierFstat (Goudet, 2005) which estimates Yang's estimators (Yang, 1998) with Weir and

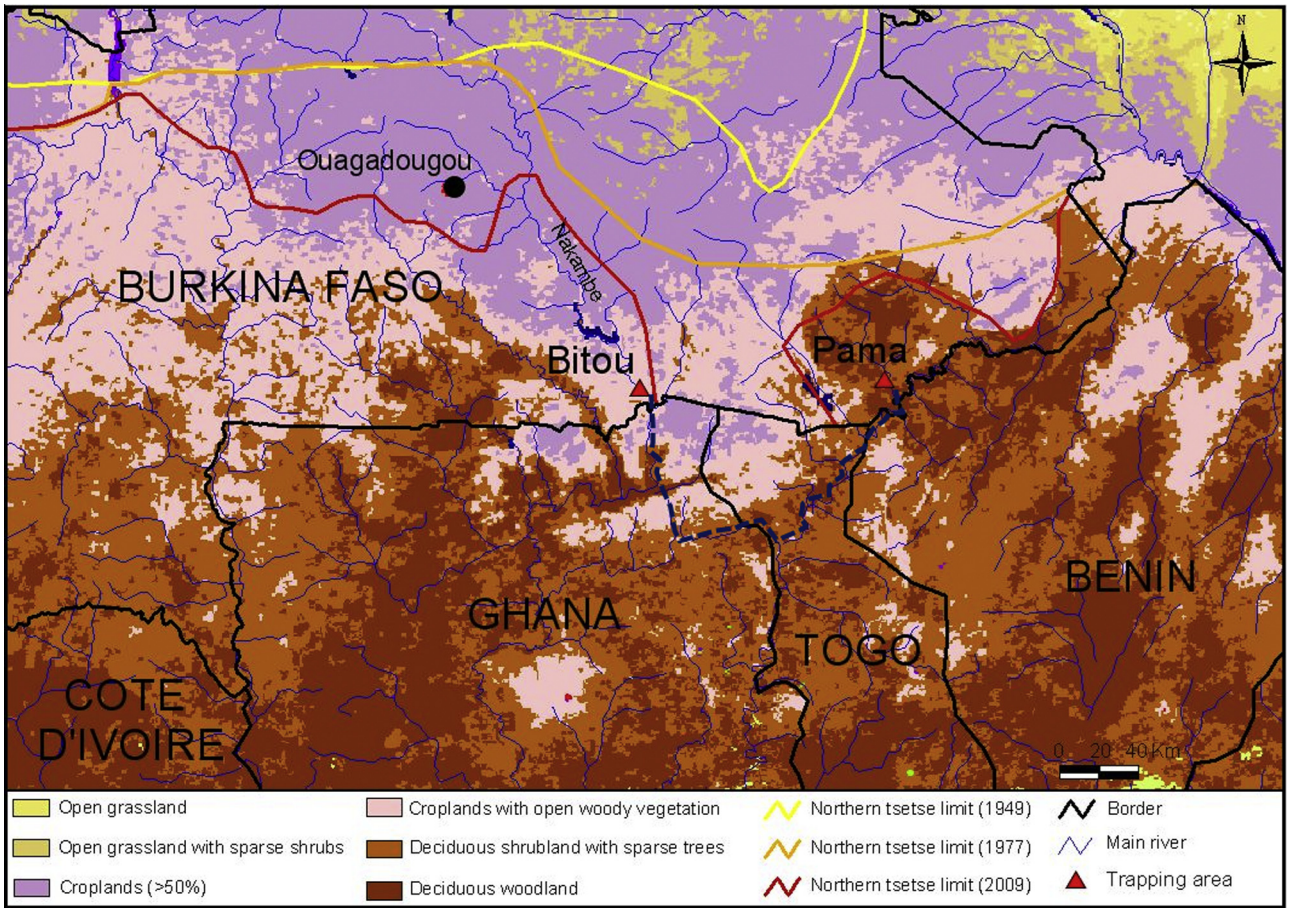

Fig. 1. Map showing the geographical location of the two sampling sites (in red) of *G. tachinoides* in Bitou and Pama, East Burkina Faso. The shortest suitable route for a tsetse fly along permanent rivers connecting the two sites is indicated with a blue dotted line. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article).